



1

SEQUENCE LISTING

<110> GORSKI, DAVID H.
WALSH, KENNETH

<120> GROWTH ARREST HOMEBOX GENE

<130> 22311/04015

<140> 09/940,673

<141> 2001-08-27

<150> 09/078,465

<151> 1998-05-14

<150> 08/203,532

<151> 1994-02-24

<160> 19

<170> PatentIn Ver. 2.1

<210> 1

<211> 2244

<212> DNA

<213> Rattus sp.

<220>

<221> CDS

<222> (197)..(1105)

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agtgaagaagt gacagcgctt ggtggacttt gggaccttcg tgaagtcttc tgcttgggaag 180

ctgagacttg catgcc atg gaa cac ccc ctc ttt ggc tgc ctg cgc agc ccc 232

Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser Pro
1 5 10

cac gcc aca gcg caa ggc ttg cac ccc ttc tcg cag tct tct ctg gcc 280

His Ala Thr Ala Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu Ala
15 20 25

ctc cat gga aga tct gac cac atg tcc tac ccc gaa ctc tcc aca tct 328

Leu His Gly Arg Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr Ser
30 35 40

tcc tcg tct tgc ata atc gcg gga tac ccc aat gag gag ggc atg ttt 376

Ser Ser Ser Cys Ile Ile Ala Gly Tyr Pro Asn Glu Glu Gly Met Phe
45 50 55 60

gcc agc cag cat cac agg ggg cac cac cac cac cac cac cac cat 424

Ala Ser Gln His His Arg Gly His His His His His His His His
65 70 75

cac cac cac cag cag cag cag cac cag gct ctg caa agc aac tgg cac	472
His His His Gln Gln Gln Gln His Gln Ala Leu Gln Ser Asn Trp His	
80 85 90	
ctc ccg cag atg tcc tcc ccg cca agc gcg gcc cgg cac agc ctt tgc	520
Leu Pro Gln Met Ser Ser Pro Pro Ser Ala Ala Arg His Ser Leu Cys	
95 100 105	
ctg cag cct gat tcc gga ggg ccc ccg gag ctg ggg agc agc cct ccg	568
Leu Gln Pro Asp Ser Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro Pro	
110 115 120	
gtc ctg tgc tcc aac tct tct agc ctg ggc tcc agc acc ccg acc gga	616
Val Leu Cys Ser Asn Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr Gly	
125 130 135 140	
gcc gcg tgc gca cca agg gat tat ggc cgt caa gcg ctg tca ccc gca	664
Ala Ala Cys Ala Pro Arg Asp Tyr Gly Arg Gln Ala Leu Ser Pro Ala	
145 150 155	
gaa gtg gag aag aga agt ggc agc aaa aga aaa agc gac agt tca gat	712
Glu Val Glu Lys Arg Ser Gly Ser Lys Arg Lys Ser Asp Ser Ser Asp	
160 165 170	
tcc cag gaa gga aat tac aag tca gaa gtg aac agc aaa cct agg aag	760
Ser Gln Glu Gly Asn Tyr Lys Ser Glu Val Asn Ser Lys Pro Arg Lys	
175 180 185	
gaa aga aca gct ttc acc aaa gag caa atc aga gaa ctt gag gca gag	808
Glu Arg Thr Ala Phe Thr Lys Glu Gln Ile Arg Glu Leu Glu Ala Glu	
190 195 200	
ttc gcc cat cat aac tat ctg acc aga ctg aga aga tat gag ata gcg	856
Phe Ala His His Asn Tyr Leu Thr Arg Leu Arg Arg Tyr Glu Ile Ala	
205 210 215 220	
gtg aac cta gac ctc act gaa aga cag gtg aaa gtg tgg ttc cag aac	904
Val Asn Leu Asp Leu Thr Glu Arg Gln Val Lys Val Trp Phe Gln Asn	
225 230 235	
agg aga atg aag tgg aag ccg gtc aag ggg gga caa caa gga gct gca	952
Arg Arg Met Lys Trp Lys Arg Val Lys Gly Gly Gln Gln Gly Ala Ala	
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gcc cga gaa aag gaa ctg gtg aat gtg aaa aag gga aca ctt ctt cca	1000
Ala Arg Glu Lys Glu Leu Val Asn Val Lys Lys Gly Thr Leu Leu Pro	
255 260 265	
tca gag ctg tca gga att ggt gca gcc acc ctc cag cag aca ggg gac	1048
Ser Glu Leu Ser Gly Ile Gly Ala Ala Thr Leu Gln Gln Thr Gly Asp	
270 275 280	
tca cta gca aat gac gac agt cgc gat agt gac cac agc tct gag cac	1096
Ser Leu Ala Asn Asp Asp Ser Arg Asp Ser Asp His Ser Ser Glu His	
285 290 295 300	
gca cac tta tgatacatag agagaccagc tccgtttctca ggaaagcacc	1145
Ala His Leu	

attgtgatgg caaatctcac ccaaaccatcg ttacatggc agatgactgt ggcagtgttg 1205
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 actaagtgcc tcttattgaa gatgcttcca cagtgaatt ggagaaagtg aacatatcta 1325
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 <213> Rattus sp.

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 Gln Gly Leu His Pro Phe Ser Gln Ser Leu Ala Leu His Gly Arg
 20 25 30
 Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr Ser Ser Ser Ser Cys
 35 40 45
 Ile Ile Ala Gly Tyr Pro Asn Glu Glu Gly Met Phe Ala Ser Gln His
 50 55 60

His	Arg	Gly	His	His	His	His	His	His	His	His	His	His	His	His	Gln
65						70					75				80
Gln	Gln	Gln	His	Gln	Ala	Leu	Gln	Ser	Asn	Trp	His	Leu	Pro	Gln	Met
				85					90					95	
Ser	Ser	Pro	Pro	Ser	Ala	Ala	Arg	His	Ser	Leu	Cys	Leu	Gln	Pro	Asp
			100					105					110		
Ser	Gly	Gly	Pro	Pro	Glu	Leu	Gly	Ser	Ser	Pro	Pro	Val	Leu	Cys	Ser
		115					120					125			
Asn	Ser	Ser	Ser	Leu	Gly	Ser	Ser	Thr	Pro	Thr	Gly	Ala	Ala	Cys	Ala
	130					135					140				
Pro	Arg	Asp	Tyr	Gly	Arg	Gln	Ala	Leu	Ser	Pro	Ala	Glu	Val	Glu	Lys
145					150					155					160
Arg	Ser	Gly	Ser	Lys	Arg	Lys	Ser	Asp	Ser	Ser	Asp	Ser	Gln	Glu	Gly
				165					170					175	
Asn	Tyr	Lys	Ser	Glu	Val	Asn	Ser	Lys	Pro	Arg	Lys	Glu	Arg	Thr	Ala
			180					185					190		
Phe	Thr	Lys	Glu	Gln	Ile	Arg	Glu	Leu	Glu	Ala	Glu	Phe	Ala	His	His
		195					200					205			
Asn	Tyr	Leu	Thr	Arg	Leu	Arg	Arg	Tyr	Glu	Ile	Ala	Val	Asn	Leu	Asp
		210				215					220				
Leu	Thr	Glu	Arg	Gln	Val	Lys	Val	Trp	Phe	Gln	Asn	Arg	Arg	Met	Lys
225					230					235					240
Trp	Lys	Arg	Val	Lys	Gly	Gly	Gln	Gln	Gly	Ala	Ala	Ala	Arg	Glu	Lys
				245					250					255	
Glu	Leu	Val	Asn	Val	Lys	Lys	Gly	Thr	Leu	Leu	Pro	Ser	Glu	Leu	Ser
			260					265					270		
Gly	Ile	Gly	Ala	Ala	Thr	Leu	Gln	Gln	Thr	Gly	Asp	Ser	Leu	Ala	Asn
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tgc	ctg	cgc	agc	cct	cac	gcc	acg	gcg	caa	ggc	ttg	cac	ccg	ttc	tcc	101
Cys	Leu	Arg	Ser	Pro	His	Ala	Thr	Ala	Gln	Gly	Leu	His	Pro	Phe	Ser	
	10					15					20					
caa	tcc	tct	ctc	gcc	ctc	cat	gga	aga	tct	gac	cat	atg	tct	tac	ccc	149
Gln	Ser	Ser	Leu	Ala	Leu	His	Gly	Arg	Ser	Asp	His	Met	Ser	Tyr	Pro	
	25					30					35					
gag	ctc	tct	act	tct	tcc	tca	tct	tgc	ata	atc	gcg	gga	tac	ccc	aac	197
Glu	Leu	Ser	Thr	Ser	Ser	Ser	Ser	Cys	Ile	Ile	Ala	Gly	Tyr	Pro	Asn	
	40				45				50						55	
gaa	gag	gac	atg	ttt	gcc	agc	cag	cat	cac	agg	ggg	cac	cac	cac	cac	245
Glu	Glu	Asp	Met	Phe	Ala	Ser	Gln	His	His	Arg	Gly	His	His	His	His	
				60					65					70		
cac	cac	cac	cat	cac	cac	cat	cag	cag	cag	cag	cac	cag	gct	ctg	caa	293
His	His	His	His	His	His	His	Gln	Gln	Gln	Gln	His	Gln	Ala	Leu	Gln	
			75				80						85			
acc	aac	tgg	cac	ctc	ccg	cag	atg	tct	tcc	cca	ccg	agt	gcg	gct	cgg	341
Thr	Asn	Trp	His	Leu	Pro	Gln	Met	Ser	Ser	Pro	Pro	Ser	Ala	Ala	Arg	
	90					95						100				
cat	agc	ctc	tgc	ctc	cag	ccc	gac	tct	gga	ggg	ccc	cca	gag	ttg	ggg	389
His	Ser	Leu	Cys	Leu	Gln	Pro	Asp	Ser	Gly	Gly	Pro	Pro	Glu	Leu	Gly	
	105				110						115					
agc	agc	ccg	ccc	gtc	ctg	tgc	tcc	aac	tct	tcc	agc	ttg	ggc	tcc	agc	437
Ser	Ser	Pro	Pro	Val	Leu	Cys	Ser	Asn	Ser	Ser	Ser	Leu	Gly	Ser	Ser	
	120				125					130					135	
acc	ccg	act	ggg	gcc	gcg	tgc	gcg	ccg	ggg	gac	tac	ggc	cgc	cag	gca	485
Thr	Pro	Thr	Gly	Ala	Ala	Cys	Ala	Pro	Gly	Asp	Tyr	Gly	Arg	Gln	Ala	
			140						145					150		
ctg	tca	cct	gcg	gag	gcg	gag	aag	cga	agc	ggc	ggc	aag	agg	aaa	agc	533
Leu	Ser	Pro	Ala	Glu	Ala	Glu	Lys	Arg	Ser	Gly	Gly	Lys	Arg	Lys	Ser	
			155					160					165			
gac	agc	tca	gac	tcc	cag	gaa	gga	aat	tac	aag	tca	gaa	gtc	aac	agc	581
Asp	Ser	Ser	Asp	Ser	Gln	Glu	Gly	Asn	Tyr	Lys	Ser	Glu	Val	Asn	Ser	
		170					175					180				
aaa	ccc	agg	aaa	gaa	agg	aca	gca	ttt	acc	aaa	gag	caa	atc	aga	gaa	629
Lys	Pro	Arg	Lys	Glu	Arg	Thr	Ala	Phe	Thr	Lys	Glu	Gln	Ile	Arg	Glu	
	185					190					195					
ctt	gaa	gca	gaa	ttt	gcc	cat	cat	aat	tat	ctc	acc	aga	ctg	agg	cga	677
Leu	Glu	Ala	Glu	Phe	Ala	His	His	Asn	Tyr	Leu	Thr	Arg	Leu	Arg	Arg	
	200				205					210					215	

tac gag ata gca gtg aat ctg gat ctc act gaa aga cag gta aaa gtc 725
 Tyr Glu Ile Ala Val Asn Leu Asp Leu Thr Glu Arg Gln Val Lys Val
 220 225 230
 tgg ttc caa aac agg cgg atg aag tgg aag agg gta aag ggt gga cag 773
 Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Arg Val Lys Gly Gly Gln
 235 240 245
 caa gga gct gcg gct cgg gaa aag gaa ctg gtg aat gtg aaa aag gga 821
 Gln Gly Ala Ala Ala Arg Glu Lys Glu Leu Val Asn Val Lys Lys Gly
 250 255 260
 aca ctt ctc cca tca gag ctg tcg gga att ggt gca gcc acc ctc cag 869
 Thr Leu Leu Pro Ser Glu Leu Ser Gly Ile Gly Ala Ala Thr Leu Gln
 265 270 275
 caa aca ggg gac tct ata gca aat gaa gac agt cac gac agt gac cac 917
 Gln Thr Gly Asp Ser Ile Ala Asn Glu Asp Ser His Asp Ser Asp His
 280 285 290 295
 agc tca gag cac gcc cac ctc tga 941
 Ser Ser Glu His Ala His Leu
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<210> 4
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 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser Pro His Ala Thr Ala
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 20 25 30
 Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr Ser Ser Ser Cys
 35 40 45
 Ile Ile Ala Gly Tyr Pro Asn Glu Glu Asp Met Phe Ala Ser Gln His
 50 55 60
 His Arg Gly His His His His His His His His His His Gln Gln
 65 70 75 80
 Gln Gln His Gln Ala Leu Gln Thr Asn Trp His Leu Pro Gln Met Ser
 85 90 95
 Ser Pro Pro Ser Ala Ala Arg His Ser Leu Cys Leu Gln Pro Asp Ser
 100 105 110
 Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro Pro Val Leu Cys Ser Asn
 115 120 125
 Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr Gly Ala Ala Cys Ala Pro
 130 135 140

Gly Asp Tyr Gly Arg Gln Ala Leu Ser Pro Ala Glu Ala Glu Lys Arg
 145 150 155 160
 Ser Gly Gly Lys Arg Lys Ser Asp Ser Ser Asp Ser Gln Glu Gly Asn
 165 170 175
 Tyr Lys Ser Glu Val Asn Ser Lys Pro Arg Lys Glu Arg Thr Ala Phe
 180 185 190
 Thr Lys Glu Gln Ile Arg Glu Leu Glu Ala Glu Phe Ala His His Asn
 195 200 205
 Tyr Leu Thr Arg Leu Arg Arg Tyr Glu Ile Ala Val Asn Leu Asp Leu
 210 215 220
 Thr Glu Arg Gln Val Lys Val Trp Phe Gln Asn Arg Arg Met Lys Trp
 225 230 235 240
 Lys Arg Val Lys Gly Gly Gln Gln Gly Ala Ala Ala Arg Glu Lys Glu
 245 250 255
 Leu Val Asn Val Lys Lys Gly Thr Leu Leu Pro Ser Glu Leu Ser Gly
 260 265 270
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 Asp Ser His Asp Ser Asp His Ser Ser Glu His Ala His Leu
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 29-mer oligonucleotide

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<210> 6
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 Primer

<220>
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<400> 6
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18

<210> 7
 <211> 30
 <212> DNA
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<220>
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<210> 8
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 <212> DNA
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<220>
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<210> 9
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 <210> 10
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